

Job Title: jcl3914 (16 letters)

Please, by all means, C&S!!!

နိဂုံး

SID: 89C4726201P

If you have any problems or questions with the results of this search please refer to the NASD FAQs.

Technical Details

Query:
Lenth = 16

Mouse over to see the define, click to show alignments

Color key for alignment scores

Score	Color
<40	Black
40-50	Dark Grey
50-60	Medium Grey
60-70	Light Grey
70-80	White
80-90	Light Green
90-100	Dark Green

Query

0 3 6 9 12 15

Legend for links to other resources: UniProt GEO Gene Structure Map Viewer

(Click headers to sort columns)

Accession	Description	Accession	Gene name	Gene length	Gene score	Gene score	Gene score	Gene score
AF192512.1	21kD leishmanin domain, 5, clone 14-24125, complete sequence	AF192512.1	21kD	322	100%	9.9	100%	
AF192512.2	21kD leishmanin domain, 5, clone 14-24125, complete sequence	AF192512.2	21kD	322	100%	9.9	100%	
AF192512.3	21kD leishmanin domain, 5, clone 14-24125, complete sequence	AF192512.3	21kD	322	100%	9.9	100%	
AF192512.4	21kD leishmanin domain, 5, clone 14-24125, complete sequence	AF192512.4	21kD	322	100%	9.9	100%	
AF192512.5	21kD leishmanin domain, 5, clone 14-24125, complete sequence	AF192512.5	21kD	322	100%	9.9	100%	
AF192512.6	21kD leishmanin domain, 5, clone 14-24125, complete sequence	AF192512.6	21kD	322	100%	9.9	100%	
AF192512.7	21kD leishmanin domain, 5, clone 14-24125, complete sequence	AF192512.7	21kD	322	100%	9.9	100%	
AF192512.8	21kD leishmanin domain, 5, clone 14-24125, complete sequence	AF192512.8	21kD	322	100%	9.9	100%	
AF192512.9	21kD leishmanin domain, 5, clone 14-24125, complete sequence	AF192512.9	21kD	322	100%	9.9	100%	
AF192512.10	21kD leishmanin domain, 5, clone 14-24125, complete sequence	AF192512.10	21kD	322	100%	9.9	100%	
AF192512.11	21kD leishmanin domain, 5, clone 14-24125, complete sequence	AF192512.11	21kD	322	100%	9.9	100%	
AF192512.12	21kD leishmanin domain, 5, clone 14-24125, complete sequence	AF192512.12	21kD	322	100%	9.9	100%	
AF192512.13	21kD leishmanin domain, 5, clone 14-24125, complete sequence	AF192512.13	21kD	322	100%	9.9	100%	
AF192512.14	21kD leishmanin domain, 5, clone 14-24125, complete sequence	AF192512.14	21kD	322	100%	9.9	100%	
AF192512.15	21kD leishmanin domain, 5, clone 14-24125, complete sequence	AF192512.15	21kD	322	100%	9.9	100%	
AF192512.16	21kD leishmanin domain, 5, clone 14-24125, complete sequence	AF192512.16	21kD	322	100%	9.9	100%	
AF192512.17	21kD leishmanin domain, 5, clone 14-24125, complete sequence	AF192512.17	21kD	322	100%	9.9	100%	
AF192512.18	21kD leishmanin domain, 5, clone 14-24125, complete sequence	AF192512.18	21kD	322	100%	9.9	100%	
AF192512.19	21kD leishmanin domain, 5, clone 14-24125, complete sequence	AF192512.19	21kD	322	100%	9.9	100%	
AF192512.20	21kD leishmanin domain, 5, clone 14-24125, complete sequence	AF192512.20	21kD	322	100%	9.9	100%	

AC010022.2	Human sapiens chromosome 15, clone D12-1252D1, complete sequence	22.2	22.2	100%	5.9	100%	
AF153452.2	Arabidopsis thaliana DNA, chromosome 4, coding fragment No. 46	22.2	22.2	100%	5.9	100%	
AF022711.1	Arabidopsis thaliana DNA, chromosome 4, BAC clone F55.H2 (F55H2) project	22.2	22.2	100%	5.9	100%	
AF022697.1	Mus musculus chromosome 15, clone RP23-220B05, complete sequence	22.2	22.2	100%	9.9	100%	
AF022692.2	Syntherisma sp. P02-6613 DNA, complete genome	22.2	112	100%	5.9	100%	
AF022691.1	Syntherisma P02-6202 glpF gene and CP2	22.2	22.2	100%	5.9	100%	
AF022690.1	Arabidopsis thaliana Atg156d0F02.H2_200 gene, complete cds	22.2	22.2	100%	5.9	100%	
AF022688.1	Oryza sativa Japonica Group genomic DNA, chromosome 6, PAC clone F04456F1	22.2	22.2	100%	5.9	100%	
AF022687.5	Oryza sativa Japonica Group genomic DNA, chromosome 6, PAC clone F04448A9	22.2	22.2	100%	5.9	100%	
AF022685.1	Cardiatus Strobilamine pennsylvanicus str. SPEN, complete genome	22.2	22.2	100%	5.9	100%	
AF022684.1	Arabidopsis thaliana full-length cDNA. Complete sequence from clone D5C176B12F11 of flowers and buds of strain col-0 or Arabidopsis thaliana (thale cress)	22.2	22.2	100%	5.9	100%	
AF022677.1	Syntherisma glr gene for gamma transporter	22.2	22.2	100%	5.9	100%	
AF022675.2	Mouse DNA sequence from clone RP23-251B14 on chromosome 2. Contains the 3' end of a novel gene, a ribosomal protein L23a (Rpl23a) pseudogene, a ribosomal-sparing enzyme C25 (Rpl23a) pseudogene, a high mobility group box 2 (Hmgb2) pseudogene and two novel genes. complete sequence	22.2	22.2	100%	5.9	100%	
AF022669.2	Oncometopis ypsilon C61-6436 (C61-6436), mRNA	22.2	22.2	99%	35	100%	
AF022667.1	Myoporum laetifolium v10L3.1, complete genome	22.2	22.2	99%	38	100%	
AF022666.1	Danio rerio str. d211-47615.5, mRNA (cDNA clone M3C-124559-MA3E-922296), complete cds	22.2	22.2	99%	38	100%	
AF022664.1	Danio rerio str. d211-47615.5, mRNA (cDNA clone M3C-124549-MA3C-922296), complete cds	22.2	22.2	99%	38	100%	
AF022663.2	Halobacterium sp. Str. 870, complete genome	22.2	22.2	99%	25	100%	
AF022661.1	Latobacterium raoultii F275 DNA, complete genome	22.2	22.2	99%	35	100%	
AF022659.1	Brugia malayi: Tubulin tyrosine ligase family protein partial mRNA	22.2	22.2	99%	38	100%	
AF022657.2	Acetabularia blattaria SP280: H82 hypophase protein partial mRNA	22.2	22.2	99%	38	100%	
AF022655.2	Acetabularia blattaria SP280: H82 NAD-dependent adenylyl dehydrogenase partial mRNA	22.2	22.2	99%	38	100%	
AF022653.2	Acetabularia blattaria SP280: H82 NAD-dependent adenylyl dehydrogenase partial mRNA	22.2	22.2	99%	38	100%	
AF022651.2	Phaeocharis raptum Str.15 hypophase protein partial mRNA	22.2	22.2	99%	25	100%	
AF022649.1	Physcomitrella patens subsp. patens predicted protein (PttPAC05W1T_145198), mRNA, partial cds	22.2	22.2	99%	25	100%	
AF022647.2	Solanum lycopersicon chromosome 5 clone C069C01F02621, complete sequence	22.2	22.2	99%	25	100%	
AF022645.2	Salvia grisea BAC clone C0261-19F1 from chromosome 2, complete sequence	22.2	22.2	99%	38	100%	
AF022643.2	Zelandish DNA sequence from clone DKEF-92625 in linkage group 5, complete sequence	22.2	22.2	99%	38	100%	
AF022641.1	Salvia grisea BAC clone C0261-19F1, complete genome	22.2	22.2	99%	25	100%	
AF022639.1	Danio rerio str. d211-47615.2 (str. d211-47615.5), mRNA (cDNA clone M3C-121767-MA3C-121769), complete cds	22.2	22.2	99%	25	100%	
AF022637.1	Canis familiaris, clone XJ-221524, complete sequence	22.2	22.2	99%	35	100%	
AF022635.2	Zelandish DNA sequence from clone DKEF-92622 in linkage group 14, complete sequence	22.2	22.2	99%	38	100%	
AF022633.2	Penaeus monodon BAC clone D261-14676 from chromosome 2, complete sequence	22.2	22.2	99%	25	100%	
AF022631.1	Latobacterium raoultii F275, complete genome	22.2	22.2	99%	25	100%	
AF022629.1	Mitsunobolus sp. M128-03029-12, whole genome shotgun sequence	22.2	22.2	99%	35	100%	
AF022627.2	Arabidopsis thaliana Impatiens beta-2 subunit family protein (At2G16550) mRNA, complete cds	22.2	22.2	99%	38	100%	
AF022625.1	Danio rerio str. d211-47615.5, mRNA (cDNA clone IMAGE:6755545), partial cds	22.2	22.2	99%	38	100%	
AF022623.1	Oryzopsis latifolia var. latifolia S-2501A hypophase protein (OHL2501A) partial mRNA	22.2	22.2	99%	38	100%	
AF022621.2	Danio Familiaris chromosome 24, clone XJ-1464, complete sequence	22.2	22.2	99%	25	100%	
AF022619.2	Penaeus monodon BAC clone C0261-19F1 from chromosome 2, complete sequence	22.2	22.2	99%	35	100%	
AF022617.2	Penaeus monodon BAC clone C0261-19F1 from chromosome 2, complete sequence	22.2	22.2	99%	35	100%	
AF022615.2	Chromola masonii chromosome 25, complete sequence	22.2	22.2	99%	38	100%	
AF022613.1	Shewanella frigidimarina HMMB-400, complete genome	22.2	22.2	99%	25	100%	
AF022611.2	Zelandish DNA sequence from clone D261-17804 in linkage group 15, complete sequence	22.2	22.2	99%	25	100%	
AF022609.1	Oryzopsis latifolia chromosome 2L, complete sequence	22.2	22.2	99%	35	100%	
AF022607.2	Oryzopsis latifolia chromosome 2L, complete sequence	22.2	22.2	99%	35	100%	
AF022605.2	Penaeus monodon BAC clone C0261-19F1 from chromosome 7, complete sequence	22.2	22.2	99%	38	100%	
AF022603.1	Halobacterium sp. Str. 870, complete genome, strain 870	22.2	22.2	99%	25	100%	
AF022601.1	Halobacterium sp. Str. 870, complete genome	22.2	22.2	99%	25	100%	
AF022599.1	Neurospora crassa D481, complete sequence	22.2	22.2	99%	35	100%	
AF022597.1	Arabidopsis thaliana clone pDNT021 Atg16600 impatiens beta-2 subunit family protein (At2G16550) mRNA, complete cds	22.2	22.2	99%	38	100%	
AF022595.1	Arabidopsis thaliana Impatiens beta-2 subunit family protein (At2G16550) mRNA, complete cds	22.2	22.2	99%	38	100%	
AF022593.2	Wallago truttaceus clone mtr1-6478, complete sequence	22.2	22.2	99%	25	100%	
AF022591.1	Latobacterium raoultii str. Str. 870 (Str. 870) genome, partial cds	22.2	22.2	99%	25	100%	
AF022589.1	Mus musculus BAC clone RP23-27121 from chromosome 16, complete sequence	22.2	22.2	99%	35	100%	
AF022587.2	Mus musculus chromosome 5, clone RP23-27121, complete sequence	22.2	22.2	99%	38	100%	
AF022585.2	Mus musculus chromosome 5, clone RP23-11921, complete sequence	22.2	22.2	99%	25	100%	
AF022583.2	Mus musculus BAC clone RP24-124K5 from chromosome 18, complete sequence	22.2	22.2	99%	35	100%	
AF022581.2	Penaeus monodon BAC clone RP24-124L6 from chromosome 7, complete sequence	22.2	22.2	99%	38	100%	
AF022579.2	Mus musculus chromosome 5, clone RP24-124H2, complete sequence	22.2	22.2	99%	38	100%	
AF022577.2	Mus musculus BAC clone RP24-124K6 from chromosome 18, complete sequence	22.2	22.2	99%	25	100%	
AF022575.2	Mus musculus strain D5761a1 chromosome 6 clone RP23-25121, complete sequence	22.2	22.2	99%	35	100%	
AF022573.2	Mus musculus chromosome 17, clone RP23-21111, complete sequence	22.2	22.2	99%	35	100%	
AF022571.2	Mus musculus BAC clone RP24-124L13 from chromosome 18, complete sequence	22.2	22.2	99%	25	100%	
AF022569.2	Mus musculus BAC clone RP23-123K19 from chromosome 18, complete sequence	22.2	22.2	99%	25	100%	
AF022567.2	Mus musculus chromosome 14, clone RP23-112M13, complete sequence	22.2	22.2	99%	35	100%	
AF022565.2	Mus musculus chromosome 10B, clone RP23-27121, complete sequence	22.2	22.2	99%	35	100%	
AF022563.2	Human sapiens PAC clone RP4-124H4 from 7, complete sequence	22.2	22.2	99%	25	100%	
AF022561.2	Human DNA sequence from clone RP4-124H4 on chromosome 2q21.1. 21.2 Contains the 3' end of the ITGA9 gene for integrin membrane protein 2A and a kinase family member 6A (KIF6A) pseudogene. complete sequence	22.2	22.2	99%	25	100%	
AF022559.2	Human DNA sequence from clone RP4-124H4 on chromosome 1. Contains the 2' end of the gene for a novel protein (P115512), a ribosomal protein L5 (RPL5) pseudogene, the EXO1 gene for exonuclease 1, the 5' end of a ribosomal protein L22a (RPL22a) pseudogene and a 3' UTR. complete sequence	22.2	22.2	99%	35	100%	
AF022557.2	Arabidopsis thaliana chromosome 2 clone T1544 map map1236, complete sequence	22.2	22.2	99%	38	100%	
AF022555.2	Arabidopsis thaliana chromosome 2 clone T1544 map map1236, complete sequence	22.2	22.2	99%	38	100%	
AF022553.2	Human sapiens XAC RP11-635A (Research Park Cancer Institute Human BAC Library) complete sequence	22.2	22.2	99%	38	100%	
AF022551.2	Tetrahodon nigronotus full-length cDNA	22.2	22.2	99%	25	100%	
AF022549.2	Tetrahodon nigronotus full-length cDNA	22.2	22.2	99%	35	100%	
AF022547.2	Oryza sativa (Japonica cultivar group) genomic DNA, chromosome 6	22.2	22.2	99%	38	100%	
AF022545.2	Chlorophyllase thylakoid protein F of strain D25767 of Chlamydomonas reinhardtii	22.2	22.2	99%	25	100%	
AF022543.2	Halobacterium sp. Str. 870, complete genome, segment 2124	22.2	22.2	99%	25	100%	
AF022541.2	Mus musculus chromosome 5, clone RP24-124H4, complete sequence	22.2	22.2	99%	35	100%	

AC003366.4	Ornithobacteria rubeirogaster, chromosome 26, region 3452-5631, BAC clone BAGR2619, complete sequence	22.2	90.2	93%	39	100%
AC003367.6	Novoripagus BAC clone SP-1497, cont 4, complete sequence	22.2	96.6	93%	20	100%
AF003491.1	Cryptosporidium parvum genome DNA, chromosome 6, PAC clone P0612607	22.2	90.2	93%	35	100%
AF003492.1	Canis troglodytes chromosome 22 clone F7B-105112, map 22, complete sequence	22.2	90.2	93%	38	100%
AF003493.1	Canis troglodytes chromosome 22 clone F7B-117K17, map 22, partial sequence, complete sequence	22.2	90.2	92%	29	100%
AF003494.6	Cryptosporidium parvum genome DNA, chromosome 8, BAC clone QJ321_P04	22.2	90.2	93%	20	100%
AF003502.1	Cryptosporidium parvum strain 6327, hypothetical protein (C0154572) partial mRNA	22.2	90.2	93%	35	100%
AF003503.1	Salmonella typhimurium DNA, clone CH01112895	22.2	96.2	93%	35	100%
AF003505.1	Shewanella woelkei MS-1, complete genome	22.2	125	93%	38	100%
AF003506.2	Novoripagus BAC clone SP24-40102 from 1a, complete sequence	22.2	90.2	92%	29	100%


Alignments

Get selected sequences

Select all


Deselect all

Distance tree of results

> [AF003493.1](#)  Canis familiaris chromosome 9, clone XE-24065, complete sequence
Length=15476


Score = 32.2 bits (15), Expect = 9.9
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 1 GTGTCAAGCTCAAGCA 16
|||||
Sbjct 101976 GTGTCAAGCTCAAGCA 161921

> [AF003495.1](#)  Canis troglodytes BAC clone W151-49614 from chromosome 7, complete sequence
Length=17954

Score = 32.2 bits (16), Expect = 9.9
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus


Query 1 GTGTCAAGCTCAAGCA 16
|||||
Sbjct 17390 GTGTCAAGCTCAAGCA 17407

> [AF003505.1](#)  Arabidopsis thaliana proline-rich family protein (ATG019570)
mRNA, complete cds
Length=2309

GENE ID: 822508, ATG019570 : proline-rich family protein [Arabidopsis thaliana]


Score = 32.2 bits (16), Expect = 9.9
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 GTGTCAAGCTCAAGCA 16
|||||
Sbjct 2090 GTGTCAAGCTCAAGCA 2111

> [AF003506.2](#)  Novoripagus BAC clone SP4-65132 from 7, complete sequence
Length=12196

Score = 32.2 bits (16), Expect = 9.9
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus


Query 1 GTGTCAAGCTCAAGCA 16
|||||
Sbjct 72053 GTGTCAAGCTCAAGCA 72069

> [AF003506.2](#)  Mus musculus 3 days ewing's sarcoma, R158N full-length enriched library, clone:0670014018 product:unclassified, full insert sequence
Length=4187

GENE ID: 81218, Trp23 : transforming growth factor beta regulated gene 3 [Mus musculus] (10 or fewer PubMed links)

Score = 32.2 bits (16), Expect = 9.9
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus


Query 1 GTGTCAAGCTCAAGCA 16
|||||
Sbjct 1630 GTGTCAAGCTCAAGCA 1645

> [AF003506.2](#)  Arabidopsis thaliana ATG18960/228712_220 mRNA, complete cds
Length=2134

GENE ID: 822502, ATG18960 : proline-rich family protein [Arabidopsis thaliana]

Score = 32.2 bits (16), Expect = 9.9
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus


Query 1 GTGTCAAGCTCAAGCA 16
|||||
Sbjct 1821 GTGTCAAGCTCAAGCA 1836

> [AF003506.2](#)  Mus musculus bone marrow stroma cell C26-7028 SR-4987 cDNA, R158N full-length enriched library, clone:0670016023 product:unclassified, full insert sequence
Length=2928

GENE ID: 81218, Trp23 : transforming growth factor beta regulated gene 3 [Mus musculus] (10 or fewer PubMed links)

Score = 32.2 bits (16), Expect = 9.9
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 1 GTGTCAAGCTCAAGCA 16
|||||

>  chr16:36063222-36063222 Oryza sativa (japonica cultivar-group) genomic DNA, chromosome
5
length=36731836

Sort alignments for this subject sequence by:

E value	Score	Percent identity	Query start position	Subject start position
---------	-------	------------------	----------------------	------------------------

features flanking this part of subject sequence:

0000_00.at.01.ste: 0000000000
0000_00.at.02.ste: 0000000000

Score = 32.3 bits (16), Expect = 9.5
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Flavj/minis

Query	1	GTGTCAGAGCCGAAACA	16
Subject	6093485	GTGTCAGAGCCGAAACA	6093470

Features flanking this part of subject sequence.
 25A91 bp at 5' end: Q006q037700
 42874 bp at 3' end: XRNA-5S ribosomal RNA

```
Score = 30.2 bits (15), Expect = 39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
```

Query 2	IGTGAAGAGCAAGCA	16
Subject 22032237	TGTCAAGAGCAAGCA	22032251

Features flanking this part of subject sequence:
16443 bp at 5' side: 020600266200
20352 bp at 3' side: 030600332300

Score = 26.2 bits (12), Expect = 612
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand-Plus/Plus

```

Query 4      TCNAAAGCCNAAACA 16
            ||| ||| ||| |||
Subject 12671354 TCNAAAGCCNAAACA 12671356

```

Features flanking this part of subject sequence:
 55721 bp at 3' end: 560500353500
 15261 bp at 3' end: 226600353500

Score = 26.3 bits (1.3), Expect = 612
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus

Query	4	TCATAGCTCATAAA	16
Subject	14396334	TCATAGCTCATAAA	14396322

features in this part of subject sequence:
1000000000

Score = 26.3 bits (13), Expect = 612
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus

```
Query 3      GTCAAGGCCAAG 15
             ||| ||| ||| |||
Subject 19754591 GTCAAGGCCAAG 19754577
```

Features flanking this part of subject sequence:
 2676 bp at 51 sides: 0000000000000000
 2700 bp at 21 sides: 0000000000000000

Score = 26.3 bits (12), Expect = 612
Identities = 13/15 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus

Query	3	GTCAAGGCTCAAG	15
Subject	Z160315	GTCAAGGCTCAAG	Z1603133

Features in this part of subject sequence:
224022211500

Score = 26.3 bits (10), Expect = 612
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand-Plus/Minus

Query 3	GTCAAGGCCAAC	15
Subject 24001305	GTCAAGGCCAAC	24001305

Features flanking this part of subject sequence:

```
11565 bp at 5' side: 23000027700
11713 bp at 3' side: 1808452.nthcsmal.502
```

Score = 26.3 bits (13), Expect = 612
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus

Query	4	TCGAAGCCAAACA	16
Subject	24976660	TCGAAGCCAAACA	24976662

Features flanking this part of subject sequence:
 22241 aa at 3' side: 550500526000
 22241 ba at 3' side: 222500000000

Score = 26.3 bits (13), Expect = 612
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Plus


Query	4	TCTAAGGCTCAACA	16
Subject	26354502	TCTAAGGCTCAACA	26354514

features in this part of subject sequence:

NCBI BLAST (16 Jan)

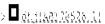
Score = 25.3 bits (13), Expect = 612
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus

Query 1 GGTCTAAGCTCAACA 14
|||||
Subject 26993691 GGTCTAAGCTCAACA 26993675

>  Human DNA sequence from clone RP11-116P24 on chromosome 1, complete sequence
Length=44737


Score = 32.1 bits (16), Expect = 9.5
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 GTCTCAAGCTCAACA 16
|||||
Subject 16716 GTCTCAAGCTCAACA 16703

>  Drosophila scripta mRNA for DNA polymerase alpha catalytic subunit, partial cds
Length=4652


Score = 32.2 bits (16), Expect = 9.9
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 GTCTCAAGCTCAACA 16
|||||
Subject 324 GTCTCAAGCTCAACA 235

>  Homo sapiens chromosome 19 clone CTD-832B9, complete sequence
Length=14526

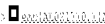
Score = 32.2 bits (16), Expect = 9.9
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 GTCTCAAGCTCAACA 16
|||||
Subject 10449 GTCTCAAGCTCAACA 10464

>  Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
Length=15975

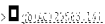
Score = 32.2 bits (16), Expect = 9.9
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 GTCTCAAGCTCAACA 16
|||||
Subject 12612 GTCTCAAGCTCAACA 12632

>  Arabidopsis thaliana DNA chromosome 4, BAC clone F2811 (F28411 project)
Length=11002

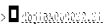
Score = 31.2 bits (16), Expect = 9.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 GTCTCAAGCTCAACA 16
|||||
Subject 53796 GTCTCAAGCTCAACA 53811

>  Mus musculus chromosome 11, clone BP23-217920, complete sequence
Length=17502

Score = 31.2 bits (16), Expect = 9.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 GTCTCAAGCTCAACA 16
|||||
Subject 88913 GTCTCAAGCTCAACA 88928

>  Zygochrysis sp. FOL 4802 DNA, complete genome
Length=357479

Best alignments for this subject sequence by:
E value SCORE EVOLUTIONARY
SIMILARITY
SIMILARITY

Features in this part of subject sequence:
AAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAA

Score = 32.2 bits (16), Expect = 9.9
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 GTCTCAAGCTCAACA 16
|||||
Subject 240613 GTCTCAAGCTCAACA 240626

Features in this part of subject sequence:
AAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAA

Score = 28.2 bits (14), Expect = 125
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Plus

Query 1 GTCTCAAGCTCAACA 14
|||||
Subject 207748 GTCTCAAGCTCAACA 207761

Features in this part of subject sequence:
AAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAA

Score = 25.3 bits (13), Expect = 612
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Plus

Query	4	TCACAGCCCAACA	15
Subject	3633571	TCACAGCCCAACA	3633559

Query	1	GTCGCAAGGCAAAACA	16
Subject	154	GTCGCAAGGCAAAACA	178

Query	1	GTGTCAAAGGCCAACA	16
Subject	1675	GTGTCAAAGGCCAACA	1090

Query	1	GTGTCAAAGCCAAACA	16
Ref	7304	GTGTCAAAGCCAAACA	7269

Query	1	GTGTCAAGCCCAACA	16
RefSeq	97994	GTGTCAAGCCCAACA	97969




Query 1	GTGTCAAGGCGAACA	16
Sbjct 442725	GTGTCAAGGCGAACA	442740


Query	1	GTGTCAAGGCAACCA	16
Subject	1937	GTGTCAAGGCAACCA	1952

Query	1	GGTGCAAGGCCAACA	16
Subject	155	SIGTCAAGGCACACA	180

Score = 32.3 bits (16), Expect = 9.5
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Search=Plus/Plus




Subject: 34120 GGTCTAAAGCTAAACA 34105

>   [GenBank:U02062.1](#)  *Drosophila yakuba* GR16496 (Dyak161636), mRNA
Length=1861


[GenBank:U02062.1](#)  *Drosophila yakuba* GR16496 gene product from transcript GR16496-RA
(*Drosophila yakuba*) (10 or fewer PubMed links)

Score = 30.2 bits (15), Expect = 35
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 2 TGTCAAGCTAAACA 16
|||||
Subject 34120 GGTCTAAAGCTAAACA 1374


>   [GenBank:U02062.1](#)  *Mycoplasma aerophilum* 15813-3, complete genome
Length=92673

Sort alignments for this subject sequence by:
E value Score RawScore Identity
Query Start Position Subject Start Position

Features in this part of subject sequence:
[GenBank:U02062.1](#)  *Mycoplasma aerophilum* 15813-3




Score = 30.2 bits (15), Expect = 35
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus


Query 1 GTTCAAGCTAAAC 15
|||||
Subject 78653 GGTCTAAAGCTAAAC 78615

Features in this part of subject sequence:
[GenBank:U02062.1](#)  *Mycoplasma aerophilum* 15813-3

Score = 25.3 bits (13), Expect = 612
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus




Query 2 TGTCAAGCTAAACA 16
|||||
Subject 684108 TGTCTAAAGCTAAAC 684174


>   [GenBank:U02062.1](#)  *Danio rerio* si.ch211-67e16.9, mRNA (cDNA clone MGC:124398 IMAGE:5037290), complete cds
Length=3763

[GenBank:U02062.1](#)  *Danio rerio* si.ch211-67e16.9 : si.ch211-67e16.9 (Danio rerio)
(10 or fewer PubMed links)

Score = 30.2 bits (15), Expect = 35
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus




Query 2 TGTCAAGCTAAACA 16
|||||
Subject 7459 TGTCAAGCTAAACA 7445

>   [GenBank:U02062.1](#)  *Danio rerio* si.ch211-67e16.9, mRNA (cDNA clone MGC:194349 IMAGE:507292), complete cds
Length=3593


[GenBank:U02062.1](#)  *Danio rerio* si.ch211-67e16.9 : si.ch211-67e16.9 (Danio rerio)
(10 or fewer PubMed links)

Score = 30.2 bits (15), Expect = 35
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query 2 TGTCAAGCTAAACA 16
|||||
Subject 3459 TGTCAAGCTAAACA 1445


>   [GenBank:U02062.1](#)  *Helicobacter pylori* Sh670, complete genome
Length=165648

Sort alignments for this subject sequence by:
E value Score RawScore Identity
Query Start Position Subject Start Position

Features in this part of subject sequence:
[GenBank:U02062.1](#)  *Helicobacter pylori* Sh670




Score = 30.2 bits (15), Expect = 35
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus


Query 2 TGTCAAGCTAAACA 16
|||||
Subject 443538 TGTCTAAAGCTAAACA 443550

Features in this part of subject sequence:
[GenBank:U02062.1](#)  *Helicobacter pylori* Sh670

Score = 25.3 bits (13), Expect = 612
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Plus

Query 4 TCAAGCTAAACA 16
|||||
Subject 1475300 TCAAGCTAAACA 1475312

>   [GenBank:U02062.1](#)  *Lactococcus reuteri* F77 DNA, complete genome
Length=201941

Features in this part of subject sequence:
[GenBank:U02062.1](#)  *Lactococcus reuteri* F77

Score = 30.2 bits (15), Expect = 35
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 2 TGTCAAGCTAAACA 16
|||||

Query	2	TGTCAGAGCCAAACA	16
Subject	1120	TGTCAGAGCCAAACA	1196

```

Query 2      TGTCAAAGCCAAACA 16
             |||||
Subject 300   TGTCAAAGCCAAACA 314

```

query 1	GTGTCAAGGTCAGAC	15
shot 1282	GTGTCAAGGTCAGAC	1276

Query	1	GTGTCAAACTCAATC	15
Subject	1292	GTGTCAAAAGCAATC	1298

```
Query 2      TGTCAAGCCCAACA 16
             |||||
Subject 406   TGTCAAGCCCAACA 592
```

Query	1	GNGTCAAAGCCAAAC	15
Subject	458	GIGTCAAAGCCAAAC	474

Query	2	TGTCAGAGCCAAACA	16
Subject	21302	TGTCAGAGCCAAACA	21288

Query	2	IGTCAAGGCCAACA	16
Subject	S102	IGTCAAGGCCAACA	8156

```
> seq105356P.121 Zebrafish DNA sequence from clone DNER-13N03 in linkage group
```


Query	2	ISGCGAAGGCCAACA	16
Subject	507	TGTGAAAGGCTAAGC	406

```
> BLASTN (blastn)
Partial cds
Length=1865
```

DATA: 55802,arch21-55816.8 ; arch21-67e16.8 (Danio rerio)
(10 or fewer PubMed links)

Score = 30.2 bits (15), Expect = 32
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query	3	TGTCAGAGCCAGACA	16
Subject	760	TGTCAGAGCCAGACA	746

> [gi|141342221.1](#) (Cryptosporidium neoformans var. neoformans B-3501A hypothetical protein (CNEi227c) partial *aspa*)
length=1545

Gene ID: 938167 (NCBI) : hypothetical protein
[Cryptococcus neoformans var. neoformans 9-35012]

```
Score = 30.2 bits (15), Expect = 39
Identical = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
```

Query	1	GTGTCAAGCCAAAC	15
Subject	1525	GTGTCAAGCCAAAC	1540

>gb|AK046251.1| Canis familiaris chromosome 2a, clone X8-0414, complete sequence
length=163990

Score = 30.2 bits (15), Expect = 39
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand-Plus/minus

Query	2	TGTCAGAGCCAAACA	16
Subject	47957	TGTCAGAGCCAAACA	47953

```
> readX(10505,1) ## Pan troglodytes BAC clone CH251-355N1 from chromosome x, complete
sequence
length=157737
```

Score = 30.2 bits (17), Expect = 39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/plus

```
Query 1      TGTCAAATCCAAACA 16
             ||| ||| ||| |||
Sbjct 68307 TGTCAAAGTCAAAACA 68321
```

```
> readAA(99000..100000)
Pen tngi-bayes BAC clone CF231-627J1? from chromosome X, complete
sequence
Length=167001
```

Sort allocations for this subject sequence by:

Primary Score Percent Identical

Every third position Subject start position

Score = 30.2 bits (15), Expect = 39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
StrandPlus/Minus

Query	2	TGTCAAGGCAACCA	16
Subject	57497	TGTCAAGGCAACCA	57498

```
Score = 26.3 bits (13), Expect = 6e-2
Identities = 12/12 (100%), Gaps = 0/13 (0%)
Strand=Plus/Plus
```

Query 1	GGGTCAAGGCCA	13
RefSeq 174195	GGGTCAAGGCCA	174207

>

Sort alignments for this subject sequence by:

E value	Score	Percent identity
Query start position	Subject start position	

Features flanking this part of subject sequence:
 1702 no at 5' side: 005515-03
 1701 no at 3' side: 005516-03

Score = 30.2 bits (15), Expect = 32
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query	3	GTCTAAGCCAAACA	16
Subject	14937065	TCTAAGCCAAACA	14937065

Features flanking this part of subject sequence.
 5045 bp at 5' side: 001145-05, isoform 5
 1101 bp at 3' side: 0020010-03

Score = 38.2 bits (14), Expect = 1e-5
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Plus

Query 1	GTGTCAGAGCCAA	14
RefSeq: 5750332	GTGTCAGAGCCAA	5750345

Features in this part of subject sequence:
CG000-02

Score = 28.2 bits (14), Expect = 155
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Plus

Query 1: TGTCTAGCTCCATC 15

Score = 30.2 bits (15), Expect = 3?
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query	3	TGTCAGAGCCAAACA	16
RefSeq	953162	TGTCAGAGCCAAACA	953168

Features in this part of subject sequence:
conserved hypothetical protein with amidohydrolase domain

Score = 26.3 bits (13), Expect = 612
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=plus/plus

```
Query 4      TCAATCCTCAACA 16
            |||||
Subject 1517629 TCAATGCTCAACA 1517641
```

> [NC_008029.1](#) Helicobacter pylori RP631, complete genome
Length=1596366

Sort alignments for this subject sequence by:

<u>E value</u>	<u>Score</u>	<u>Percent identity</u>
		<u>Query start position</u> <u>Subject start position</u>

Features in this part of subject sequence:
o/longend/men/Idexa I

Score = 30.2 bits (15), Expect. = 35
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query	2	TGTCAAAGCTAAACA	16
Subject	458a16	TGTCAAAGCTAAACA	458a22

features in this part of subject sequence:
hypothetical, possible

Score = 28.3 bits (13), Expect = 61.2
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus

Query	9	TCATAGGCAACCA	16
Subject	1488867	TCATAGGCAACCA	1488865

Mitoagcis gallinaceo 07491 genomic sequences
 length=1050

Score = 30.2 bits (15), Expect = 39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query 1	GTGTCAAGCCAAAC	15
Ref: 504	GTGTCAAGCCAAAC	590

▣ [AB024650.1](#) Arabidopsis thaliana clone pEX1021-At2g16560 importin beta-2
summit family protein (At2g16560), mRNA, complete cds
Length=1518

Gene ID: 204159 At2G18960 ; Isopentenyl beta-2 subunit family protein
[Arabidopsis thaliana]

Score = 30.2 bits (15), Expect = 35
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query	2	TTCTCAAGGCTAACA	16
Subject	567	TTCTCAAGGCTAACA	498

> [refseq:NM_127449.1](#) Acetabularia thaliana importin beta-3 subunit family protein (AT7G09000)
mRNA, complete cds
length=1644

Gene ID: [S16125.AT2G16150](#) ; importin beta-2 subunit family protein
[*Arabidopsis thaliana*]

Score = 30.2 bits (15), Expect = 39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query	2	IGTCRAAGGCCAAACA	18
RefSeq	456	TGTCRAAGGCCAAACA	442

```
>  https://www.ncbi.nlm.nih.gov/nuclot/118506 Nadinso truncatula clone xthl-54n13, complete sequence  
length=118506
```

Score = 30.2 bits (15), Expect = 39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query	2	TGTCAAAGTCAACA	16
Subject	69686	TGTCAGAGGCAACA	89672

> [U04620](#) *Lactococcus reuteri* actin-like ATPase (iclA) gene, partial cds
length=348

Score = 30.2 bits (10), Expect = 35
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

```

Query 2      TGTCTAAGCCCAACA 16
             |||||
Short 275    TGTCTAAGCCCAACA 289

```

>[U01661.1](#) Mus musculus BAC clone RP22-167121 from chromosome 16, complete sequence
Length=21870

Score = 30.2 bits (15), Expect = .39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query 2 TGTCAAGGCTAAGCA 16
+ + + + +
Sbjct 150429 TGTCAAGGCTAAGCA 150415

>[U01662.1](#) Mus musculus chromosome 3, clone RP23-312117, complete sequence
Length=214261

Score = 30.2 bits (15), Expect = .39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query 2 TGTCAAGGCTAAGCA 16
+ + + + +
Sbjct 137260 TGTCAAGGCTAAGCA 137266

>[U01663.1](#) Mus musculus chromosome 5, clone RP23-015813, complete sequence
Length=209590

Score = 30.2 bits (15), Expect = .39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query 2 TGTCAAGGCTAAGCA 16
+ + + + +
Sbjct 35001 TGTCAAGGCTAAGCA 35013

>[U01664.1](#) Mus musculus BAC clone RP24-30480 from chromosome 18, complete sequence
Length=219075

Score = 30.2 bits (15), Expect = .39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query 2 TGTCAAGGCTAAGCA 16
+ + + + +
Sbjct 95870 TGTCAAGGCTAAGCA 95884

>[U01665.1](#) Pan troglodytes BAC clone SP43-55016 from chromosome 7, complete sequence
Length=153029

Score = 30.2 bits (15), Expect = .39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query 1 GTGTCAAGGCTAAGC 15
+ + + + +
Sbjct 58116 GTGTCAAGGCTAAGC 58102

>[U01666.1](#) Mus musculus chromosome 5, clone SP24-20482, complete sequence
Length=18602

Score = 30.2 bits (15), Expect = .39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 2 TGTCAAGGCTAAGCA 16
+ + + + +
Sbjct 109506 TGTCAAGGCTAAGCA 109520

>[U01667.1](#) Mus musculus BAC clone RP24-34290 from chromosome 18, complete sequence
Length=206816

Score = 30.2 bits (15), Expect = .39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query 2 TGTCAAGGCTAAGCA 16
+ + + + +
Sbjct 70260 TGTCAAGGCTAAGCA 70276

>[U01668.1](#) Mus musculus strain C57BL/6 chromosome 6 clone RP23-25811, complete sequence
Length=212366

Score = 30.2 bits (15), Expect = .39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query 2 TGTCAAGGCTAAGCA 16
+ + + + +
Sbjct 55825 TGTCAAGGCTAAGCA 55811

>[U01669.1](#) Mus musculus chromosome 17, clone RP23-211911, complete sequence
Length=158819

Score = 30.2 bits (15), Expect = .39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus



Query 2 TGTCAAGGCTAAGCA 16
+ + + + +
Sbjct 153020 TGTCAAGGCTAAGCA 153016

>[U01670.1](#) Mus musculus BAC clone RP24-242015 from chromosome 18, complete sequence
Length=16726

Score = 30.2 bits (15), Expect = .39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus



Query 2 TGTCAAGGCTAAGCA 16
+ + + + +

Subject: 145543 TGTCTAAGCTCAACA 145543

>   Mus musculus BAC clone RP23-195K10 from chromosome 1B, complete sequence
Length=61868



Score = 30.2 bits (15), Expect = .35
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query 1 TGTCTAAGCTCAACA 16
|||||
Subject 51686 TGTCTAAGCTCAACA 61872

>   Mus musculus chromosome 1B, clone RP23-312K23, complete sequence
Length=62456

Score = 30.2 bits (15), Expect = .35
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query 1 TGTCTAAGCTCAACA 16
|||||
Subject 145583 TGTCTAAGCTCAACA 145585

>   Mus musculus chromosome 1B clone RP23-270L12, complete sequence
Length=61872



Sort alignments for this subject sequence by:
E value Score Maximal Identity
Query Start Position RefSeq Name Position

Score = 30.2 bits (15), Expect = .35
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 1 TGTCTAAGCTCAACA 16
|||||
Subject 57752 TGTCTAAGCTCAACA 57756



Score = 26.8 bits (13), Expect = .612
Identities = 13/15 (86%), Gaps = 0/13 (0%)
Strand=Plus/Minus

Query 1 TGTCTAAGCTCAACA 16
|||||
Subject 155479 TGTCTAAGCTCAACA 155487

>   Homo sapiens BAC clone RP4-655C4 from 7, complete sequence
Length=105081



Score = 39.2 bits (15), Expect = .39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 1 TGTCTAAGCTCAACA 16
|||||
Subject 57750 TGTCTAAGCTCAACA 57754

>   Human DNA sequence from clone RP4-686K21 on chromosome 1. Contains the 3' end of the 11024 gene for integral membrane protein 1A and a kinesin family member 9A (KIF9A) pseudogene. complete sequence
Length=70855



Score = 30.2 bits (15), Expect = .35
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query 1 TGTCTAAGCTCAACA 16
|||||
Subject 55852 TGTCTAAGCTCAACA 55858

>   Human DNA sequence from clone RP11-557N16 on chromosome 1. Contains the 5' end of the gene for a novel protein (PLOC6515), a ribosomal protein L8 (RPL8) pseudogene. The EXO1 gene for exonuclease 1, the 5' end of a ribosomal protein L73a (RPL73a) pseudogene and a CpG island, complete sequence
Length=143967



Score = 39.2 bits (15), Expect = .39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 1 TGTCTAAGCTCAACA 16
|||||
Subject 55096 TGTCTAAGCTCAACA 55112

>   Arabidopsis thaliana chromosome 3 clone T15014 map m1398, complete sequence
Length=114861



Score = 39.2 bits (15), Expect = .39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 1 TGTCTAAGCTCAACA 16
|||||
Subject 70021 TGTCTAAGCTCAACA 70035

>   Arabidopsis thaliana chromosome 3 clone T13A24 map m1398, complete sequence
Length=83861

Score = 39.2 bits (15), Expect = .39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus





















Query 1 TGTCTAAGCTCAACA 16
|||||
Subject 72919 TGTCTAAGCTCAACA 72925

>   Homo sapiens X 56C RP11-605J4 (Roswell Park Cancer Institute)

Length=54425

Score = 30.2 bits (15), Expect = 39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 2 TGTCAAGCCCAACA 16
+ + + + +
Subject 29782 TGTCAAGCCCAACA 29789

>                    

>[DQ486081.2](#) [Drosophila melanogaster](#), chromosome 2R, region 5442-5461, 240 clone BACR06115, complete sequence
Length=16050

Score = 39.2 bits (15), Expect = .39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 2 TGTCAAGCTCAAGC 16
|||||
Sbjct 145626 TGTCAAGCTCAAGC 145650

>[AF122810.5](#) [Homo sapiens](#) BAC clone KP11-4971 from 4, complete sequence
Length=47574

Sort alignments for this subject sequence by:
E value Score EExpect LIdentical
Query Start Position Subject Start Offset GC

Score = 39.2 bits (15), Expect = .39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 2 TGTCAAGCTCAAGC 16
|||||
Sbjct 40534 TGTCAAGCTCAAGC 40540

Score = 26.7 bits (11), Expect = .612
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Plus

Query 4 TCAAGCTCAAGC 16
|||||
Sbjct 78511 TCAAGCTCAAGC 78513

>[AF122810.5](#) [Oryza sativa](#) Japonica Group genomic DNA, chromosome 5, BAC clone:PB12307
Length=82546

Score = 39.2 bits (15), Expect = .39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 2 TGTCAAGCTCAAGC 16
|||||
Sbjct 70110 TGTCAAGCTCAAGC 70114

>[AF122810.5](#) [Pan troglodytes](#) chromosome 22 clone:PTB-105612, map 22, complete sequences
Length=41704

Score = 39.2 bits (15), Expect = .39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query 2 TGTCAAGCTCAAGC 16
|||||
Sbjct 100570 TGTCAAGCTCAAGC 100556

>[AF122810.5](#) [Pan troglodytes](#) chromosome 22 clone:PTB-117517, map 22, partial sequences, complete sequence
Length=12490

Score = 39.2 bits (15), Expect = .39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 2 TGTCAAGCTCAAGC 15
|||||
Sbjct 42990 TGTCAAGCTCAAGC 42994

>[DQ486081.2](#) [Oryza sativa](#) Japonica Group genomic DNA, chromosome 8, BAC clone:AV1221_504
Length=13967

Score = 39.2 bits (15), Expect = .39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 2 TGTCAAGCTCAAGC 16
|||||
Sbjct 103015 TGTCAAGCTCAAGC 103029

>[U01491.1](#) [Cryptococcus neoformans](#) var. [neoformans](#) JEC21 hypothetical protein (CNE04576), partial cDNA
Length=1708

[GenBank](#) [EMBL](#) [GenBank](#) [EMBL](#) : hypothetical protein
[Cryptococcus neoformans var. neoformans JEC21] (10 or fewer PubMed links)

Score = 39.2 bits (15), Expect = .39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 1 GTGTCAAGCTCAAGC 15
|||||
Sbjct 1652 GTGTCAAGCTCAAGC 1656

>[X60443.1](#) [Galus gallus](#) furnished cDNA, clone CH87118g23
Length=1787

Score = 39.2 bits (15), Expect = .39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query 2 TGTCAAGCTCAAGC 16
|||||
Sbjct 942 TGTCAAGCTCAAGC 940

>[AF122810.5](#) [Shewanella oneidensis](#) MR-1, complete genome
Length=496963

Sort alignments for this subject sequence by:
E value Score EExpect LIdentical

Features in this part of subject sequence:
TGGTCAAGCTCAAGCA
Score = 30.2 bits (15), Expect = 39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query 2 TGTCAAGCTCAAGCA 16
|||||
Subject 228375 TGTCAAGCTCAAGCA 228381

Features in this part of subject sequence:
TGGTCAAGCTCAAGCA
Score = 25.3 bits (13), Expect = 612
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Plus

Query 4 TCAAGCTCAAGCA 16
|||||
Subject 2989642 TCAAGCTCAAGCA 2989654

Features in this part of subject sequence:
TCAAGCTCAAGCA
Score = 26.7 bits (13), Expect = 612
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Plus

Query 4 TCAAGCTCAAGCA 16
|||||
Subject 3304711 TCAAGCTCAAGCA 3304723

Features in this part of subject sequence:
TCAAGCTCAAGCA
Score = 25.3 bits (13), Expect = 612
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus

Query 2 TGTCAAGCTCAAGCA 16
|||||
Subject 3984394 TGTCAAGCTCAAGCA 3984402

Features in this part of subject sequence:
TGTCAAGCTCAAGCA
Score = 26.3 bits (13), Expect = 612
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Plus

Query 4 TCAAGCTCAAGCA 16
|||||
Subject 4507228 TCAAGCTCAAGCA 4507238

>gqkac15123.21 [Mus musculus BAC clone RP24-145B22 from 16, complete sequence
Length=149772

Score = 30.2 bits (15), Expect = 39
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 2 TGTCAAGCTCAAGCA 16
|||||
Subject 102395 TGTCAAGCTCAAGCA 102379

Get selected sequences Select all Deselected Distance tree of results

Database: All GenBank/EMBL/DBJ+PDB sequences (but no CDS, tRNA,
GSS, environmental samples or phage 0, 1 or 2 HGB sequences)
Posted date: Aug 16, 2008 5:48 PM
Number of letters in database: 1,013,620,335
Number of sequences in database: 7,346,645

Lambda E H
1.37 0.711 1.31
Gapped
Lambda E H
1.37 0.711 1.31
Matrix: blastn matrix: 1-2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 7348665
Number of hits to DB: 875149
Number of extensions: 3684592
Number of successful extensions: 17641
Number of sequences better than 1000: 523
Number of HSP's better than 1000 without gapping: 0
Number of HSP's gapped: 13441
Number of HSP's successfully gapped: 545
Length of query: 16
Length of database: 24756267437
Length adjustment: 14
Effective length of query: 1
Effective length of database: 26953502127
Effective search space: 49307004754
Effective search space used: 49307004254
A: 5
Z1: 11 (21.8 bits)
Z2: 15 (29.7 bits)
Z3: 50 (59.1 bits)
Z4: 11 (22.3 bits)
Z5: 13 (28.3 bits)